S19 Table: Model of association between global ancestry and BMI, including interaction with type-2 diabetes.

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| Model 1: linear regression between BMI and covariates |
| variables | estimate | std. error | t | p | R2 | df |
| intercept | 34.1237 | 0.7376 | 46.264 | <2×10-16 | 0.0212 | 3401 |
| age (at baseline) | -0.0832 | 0.0131 | -6.378 | 2.10×10-10 |
| Sex | -0.7239 | 0.2006 | -3.608 | 3.13×10-4 |
| edu4\* | -1.2995 | 0.2347 | -5.538 | 3.29×10-8 |
| Model 2: linear regression between rank-based inversed residual and global ancestry |
| intercept | -0.4586 | 0.0628 | -7.307 | 3.46×10-13 | 0.1738 | 3080 |
| PNS | 0.8330 | 0.1110 | 7.506 | 7.95×10-14 |
| EAS | -0.5164 | 0.0867 | -5.954 | 2.91×10-9 |
| AFR | 1.1126 | 0.7844 | 1.418 | 0.1562 |
| t2d | 0.9937 | 0.1087 | 9.139 | <2×10-16 |
| PNS:t2d | -0.6338 | 0.1787 | -3.546 | 0.0004 |
| EAS:t2d | -0.1846 | 0.1419 | -1.301 | 0.1933 |
| AFR:t2d | -0.5000 | 1.2382 | -0.404 | 0.6864 |

Model 1 models the non-genetic covariates according to the heuristic described in the **Methods**, except for type-2 diabetes status. The residual from model 1 was then inverse normalized and tested in model 2, which includes global ancestries, type-2 diabetes status, and interactions between global ancestries and type-2 diabetes status. \* edu4 was a binary variable created from the original categorical variable of education status by grouping levels 1,2,3 and coded 0, while education status level 4 was coded as 1. This was done because there were no significant associations between education levels 1 through 3 and BMI.